



## SEQUENCE LISTING

&lt;110&gt; NIPPON SHOKUBAI CO., LTD.

NATIONAL INSTITUTE OF TECHNOLOGY AND EVALUATION

&lt;120&gt; Novel Modified S-Hydroxynitrile lyase

&lt;130&gt; PH-2387-PCT

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; JP 2004-105642

&lt;151&gt; 2004-03-31

&lt;160&gt; 44

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Manihot esculenta

&lt;220&gt;

&lt;223&gt; Inventor: Ichige, Eita; Semba, Hisashi; Shijuku, Toshiaki; Harayama, Shigeaki

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(777)

&lt;400&gt; 1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | ggt | act | gca | cac | ttc | ggt | ctg | att | cac | acc | att | tgt | cac | ggc | gca | 48 |
| Met | Val | Thr | Ala | His | Phe | Val | Leu | Ile | His | Thr | Ile | Cys | His | Gly | Ala |    |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| tgg | att | tgg | cac | aaa | ctg | aaa | ccg | gcc | ctg | gaa | cgt | gct | ggc | cac | aaa | 96 |
| Trp | Ile | Trp | His | Lys | Leu | Lys | Pro | Ala | Leu | Glu | Arg | Ala | Gly | His | Lys |    |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ggt | act | gca | ctg | gac | atg | gca | gcc | agt | ggc | att | gac | ccg | cgt | caa | att | 144 |
| Val | Thr | Ala | Leu | Asp | Met | Ala | Ala | Ser | Gly | Ile | Asp | Pro | Arg | Gln | Ile |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gaa | cag | atc | aac | tct | ttc | gat | gaa | tac | tct | gaa | ccg | ctg | ctg | act | ttc | 192 |
| Glu | Gln | Ile | Asn | Ser | Phe | Asp | Glu | Tyr | Ser | Glu | Pro | Leu | Leu | Thr | Phe |     |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ctg | gaa | aaa | ctg | ccg | caa | ggc | gaa | aag | ggt | atc | att | ggt | ggt | gaa | agc | 240 |
| Leu | Glu | Lys | Leu | Pro | Gln | Gly | Glu | Lys | Val | Ile | Ile | Val | Gly | Glu | Ser |     |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tgt | gca | ggc | ctg | aac | att | gct | att | gct | gct | gat | cgt | tac | ggt | gac | aaa | 288 |
| Cys | Ala | Gly | Leu | Asn | Ile | Ala | Ile | Ala | Ala | Asp | Arg | Tyr | Val | Asp | Lys |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255

tac gct taa 777  
 Tyr Ala

<210> 2  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<400> 2  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

|   |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |
| Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser |     |     |     |     |     |
| 65  |     | 70  |     | 75  | 80  |
| Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys |     |     |     |     |     |
|   | 85  |     | 90  |     | 95  |
| Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His |     |     |     |     |     |
|   | 100 |     | 105 |     | 110 |
| Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp |     |     |     |     |     |
|   | 115 |     | 120 |     | 125 |
| Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile |     |     |     |     |     |
|   | 130 |     | 135 |     | 140 |
| Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr |     |     |     |     |     |
| 145   |     | 150 |     | 155 | 160 |
| Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys |     |     |     |     |     |
|   | 165 |     | 170 |     | 175 |
| Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu |     |     |     |     |     |
|   | 180 |     | 185 |     | 190 |
| Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp |     |     |     |     |     |
|   | 195 |     | 200 |     | 205 |
| Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys |     |     |     |     |     |
|   | 210 |     | 215 |     | 220 |
| Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu |     |     |     |     |     |
| 225   |     | 230 |     | 235 | 240 |
| Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala |     |     |     |     |     |
|   | 245 |     | 250 |     | 255 |
| Tyr Ala   |     |     |     |     |     |

<210> 3  
 <211> 774  
 <212> DNA  
 <213> Hevea brasiliensis

<220>  
 <221> CDS  
 <222> (1)..(774)

|   |     |
|---|-----|
| <400> 3   |     |
| atg gca ttc gct cat ttt gtt ctt att cat acc ata tgc cac ggt gca | 48  |
| Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala |     |
| 1 5 10 15   |     |
|   |     |
| tgg att tgg cac aag ctc aaa ccc ctc ctt gag gca ctt ggc cac aag | 96  |
| Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys |     |
| 20 25 30  |     |
|   |     |
| gtt act gca ctg gac ctt gca gca agc ggc gtt gac cca agg caa att | 144 |
| Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile |     |
| 35 40 45  |     |
|   |     |
| gag gag att ggc tca ttt gat gag tat tct gaa ccc ttg ttg acg ttc | 192 |
| Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe |     |
| 50 55 60  |     |
|   |     |
| ttg gag gca ctc cct cca ggg gaa aag gtg att ctg gtt ggc gag agc | 240 |
| Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser |     |

| 65  | 70  | 75  | 80  |     |
|---|-----|-----|-----|-----|
| tgt gga gga ctc aat ata gca att gct gct gat aaa tac tgt gaa aag |     |     |     | 288 |
| Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys |     |     |     |     |
|   | 85  | 90  | 95  |     |
| att gca gct gct gtt ttc cac aat tca gta ttg cca gac acc gag cac |     |     |     | 336 |
| Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His |     |     |     |     |
|   | 100 | 105 | 110 |     |
| tgc cca tct tac gtc gtg gat aag ctc atg gag gtg ttt ccc gac tgg |     |     |     | 384 |
| Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp |     |     |     |     |
|   | 115 | 120 | 125 |     |
| aaa gac acc acg tat ttt acg tac act aaa gat ggc aag gag ata act |     |     |     | 432 |
| Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr |     |     |     |     |
|   | 130 | 135 | 140 |     |
| gga ttg aaa ctg ggc ttc acg ctt ctg agg gaa aat tta tat acc ctt |     |     |     | 480 |
| Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu |     |     |     |     |
|   | 145 | 150 | 155 | 160 |
| tgc ggt cct gag gaa tat gaa ctg gcg aag atg ttg aca agg aag gga |     |     |     | 528 |
| Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly |     |     |     |     |
|   | 165 | 170 | 175 |     |
| tca tta ttt caa aat att tta gct aag cga cca ttc ttc act aag gaa |     |     |     | 576 |
| Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu |     |     |     |     |
|   | 180 | 185 | 190 |     |
| ggt tac gga tcg att aag aaa att tat gtg tgg acc gac caa gac gaa |     |     |     | 624 |
| Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu |     |     |     |     |
|   | 195 | 200 | 205 |     |
| ata ttt tta cct gaa ttt caa ctc tgg caa ata gaa aac tat aaa cca |     |     |     | 672 |
| Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro |     |     |     |     |
|   | 210 | 215 | 220 |     |
| gac aag gtt tat aag gtc gaa ggt gga gat cat aaa ttg cag ctt aca |     |     |     | 720 |
| Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr |     |     |     |     |
|   | 225 | 230 | 235 | 240 |
| aag act aag gag atc gct gaa att ctc caa gag gtg gct gat acc tat |     |     |     | 768 |
| Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr |     |     |     |     |
|   | 245 | 250 | 255 |     |
| aat tga   |     |     |     | 774 |
| Asn   |     |     |     |     |

<210> 4

<211> 257

<212> PRT

<213> Hevea brasiliensis

<400> 4

Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |  |  |
| Trp | Ile | Trp | His | Lys | Leu | Lys | Pro | Leu | Leu | Glu | Ala | Leu | Gly | His | Lys |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Val | Thr | Ala | Leu | Asp | Leu | Ala | Ala | Ser | Gly | Val | Asp | Pro | Arg | Gln | Ile |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Glu | Glu | Ile | Gly | Ser | Phe | Asp | Glu | Tyr | Ser | Glu | Pro | Leu | Leu | Thr | Phe |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |
| Leu | Glu | Ala | Leu | Pro | Pro | Gly | Glu | Lys | Val | Ile | Leu | Val | Gly | Glu | Ser |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |  |
| Cys | Gly | Gly | Leu | Asn | Ile | Ala | Ile | Ala | Ala | Asp | Lys | Tyr | Cys | Glu | Lys |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Ile | Ala | Ala | Ala | Val | Phe | His | Asn | Ser | Val | Leu | Pro | Asp | Thr | Glu | His |  |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |  |
| Cys | Pro | Ser | Tyr | Val | Val | Asp | Lys | Leu | Met | Glu | Val | Phe | Pro | Asp | Trp |  |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |  |  |
| Lys | Asp | Thr | Thr | Tyr | Phe | Thr | Tyr | Thr | Lys | Asp | Gly | Lys | Glu | Ile | Thr |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Gly | Leu | Lys | Leu | Gly | Phe | Thr | Leu | Leu | Arg | Glu | Asn | Leu | Tyr | Thr | Leu |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Cys | Gly | Pro | Glu | Glu | Tyr | Glu | Leu | Ala | Lys | Met | Leu | Thr | Arg | Lys | Gly |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |  |
| Ser | Leu | Phe | Gln | Asn | Ile | Leu | Ala | Lys | Arg | Pro | Phe | Phe | Thr | Lys | Glu |  |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |  |  |
| Gly | Tyr | Gly | Ser | Ile | Lys | Lys | Ile | Tyr | Val | Trp | Thr | Asp | Gln | Asp | Glu |  |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |  |
| Ile | Phe | Leu | Pro | Glu | Phe | Gln | Leu | Trp | Gln | Ile | Glu | Asn | Tyr | Lys | Pro |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |  |  |
| Asp | Lys | Val | Tyr | Lys | Val | Glu | Gly | Gly | Asp | His | Lys | Leu | Gln | Leu | Thr |  |  |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |  |  |
| Lys | Thr | Lys | Glu | Ile | Ala | Glu | Ile | Leu | Gln | Glu | Val | Ala | Asp | Thr | Tyr |  |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |  |

Asn

<210> 5

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<223> cDNA coding for Modified SHNL involving  
a replacement of Gly by Asp at position 165

<220>

<221> CDS

<222> (1)..(777)

<400> 5

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | gtt | act | gca | cac | ttc | gtt | ctg | att | cac | acc | att | tgt | cac | ggc | gca | 48 |
| Met | Val | Thr | Ala | His | Phe | Val | Leu | Ile | His | Thr | Ile | Cys | His | Gly | Ala |    |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| tgg | att | tgg | cac | aaa | ctg | aaa | ccg | gcc | ctg | gaa | cgt | gct | ggc | cac | aaa | 96 |
| Trp | Ile | Trp | His | Lys | Leu | Lys | Pro | Ala | Leu | Glu | Arg | Ala | Gly | His | Lys |    |
|     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |    |

|   |     |
|---|-----|
| gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att | 144 |
| Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile |     |
| 35 40 45  |     |
| gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc | 192 |
| Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe |     |
| 50 55 60  |     |
| ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc | 240 |
| Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser |     |
| 65 70 75 80   |     |
| tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa | 288 |
| Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys |     |
| 85 90 95  |     |
| att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac | 336 |
| Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His |     |
| 100 105 110   |     |
| agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg | 384 |
| Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp |     |
| 115 120 125   |     |
| cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc | 432 |
| Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile |     |
| 130 135 140   |     |
| act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc | 480 |
| Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr |     |
| 145 150 155 160   |     |
| aaa tgc act gat gac gaa tat gaa ctg gca aaa atg gtt atg cgc aag | 528 |
| Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys |     |
| 165 170 175   |     |
| ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa | 576 |
| Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu |     |
| 180 185 190   |     |
| aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac | 624 |
| Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp |     |
| 195 200 205   |     |
| aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa | 672 |
| Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys |     |
| 210 215 220   |     |
| ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg | 720 |
| Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu |     |
| 225 230 235 240   |     |
| aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca | 768 |
| Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala |     |
| 245 250 255   |     |
| tac gct taa   | 777 |

Tyr Ala

<210> 6  
<211> 258  
<212> PRT  
<213> Manihot esculenta

<220>  
<223> Modified SHNL involving  
a replacement of Gly by Asp at position 165

<400> 6  
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
1 5 10 15  
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
20 25 30  
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
35 40 45  
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
50 55 60  
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
65 70 75 80  
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
85 90 95  
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
100 105 110  
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
115 120 125  
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
130 135 140  
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
145 150 155 160  
Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
165 170 175  
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
180 185 190  
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
195 200 205  
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
210 215 220  
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
225 230 235 240  
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
245 250 255

Tyr Ala

<210> 7  
<211> 777  
<212> DNA  
<213> Manihot esculenta

<220>  
<221> CDS  
<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving  
a replacement of Gly by Glu at position 165

<400> 7

|   |     |
|---|-----|
| atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca | 48  |
| Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala |     |
| 1 5 10 15   |     |
|   |     |
| tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa | 96  |
| Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys |     |
| 20 25 30  |     |
|   |     |
| gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att | 144 |
| Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile |     |
| 35 40 45  |     |
|   |     |
| gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc | 192 |
| Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe |     |
| 50 55 60  |     |
|   |     |
| ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc | 240 |
| Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser |     |
| 65 70 75 80   |     |
|   |     |
| tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa | 288 |
| Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys |     |
| 85 90 95  |     |
|   |     |
| att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac | 336 |
| Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His |     |
| 100 105 110   |     |
|   |     |
| agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg | 384 |
| Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp |     |
| 115 120 125   |     |
|   |     |
| cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc | 432 |
| Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile |     |
| 130 135 140   |     |
|   |     |
| act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc | 480 |
| Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr |     |
| 145 150 155 160   |     |
|   |     |
| aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg gtt atg cgc aag | 528 |
| Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys |     |
| 165 170 175   |     |
|   |     |
| ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa | 576 |
| Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu |     |
| 180 185 190   |     |
|   |     |
| aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac | 624 |
| Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp |     |
| 195 200 205   |     |



|   |     |
|---|-----|
| aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa | 672 |
| Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys |     |
| 210 215 220   |     |
|   |     |
| ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg | 720 |
| Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu |     |
| 225 230 235 240   |     |
|   |     |
| aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca | 768 |
| Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala |     |
| 245 250 255   |     |
|   |     |
| tac gct taa   | 777 |
| Tyr Ala   |     |

<210> 8  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
       a replacement of Gly by Glu at position 165

<400> 8

|   |  |
|---|--|
| Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala |  |
| 1 5 10 15   |  |
| Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys |  |
| 20 25 30  |  |
| Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile |  |
| 35 40 45  |  |
| Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe |  |
| 50 55 60  |  |
| Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser |  |
| 65 70 75 80   |  |
| Cys Ala Gly Leu Asn Ile Ala Ile Ala Asp Arg Tyr Val Asp Lys     |  |
| 85 90 95  |  |
| Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His |  |
| 100 105 110   |  |
| Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp |  |
| 115 120 125   |  |
| Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile |  |
| 130 135 140   |  |
| Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr |  |
| 145 150 155 160   |  |
| Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys |  |
| 165 170 175   |  |
| Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu |  |
| 180 185 190   |  |
| Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp |  |
| 195 200 205   |  |
| Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys |  |
| 210 215 220   |  |
| Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu |  |
| 225 230 235 240   |  |



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

cgtgaaaacc tggtcaccaa atgcactgat gaagaatatg aactggcaaa aatg 54

<210> 14

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14

catttttgcc agttcatatt cttcatcagt gcatttggtg aacaggtttt cacg 54

<210> 15

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving  
a replacement of Val by Leu at position 173

<400> 15

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | ggt | act | gca | cac | ttc | ggt | ctg | att | cac | acc | att | tgt | cac | ggc | gca | 48 |
| Met | Val | Thr | Ala | His | Phe | Val | Leu | Ile | His | Thr | Ile | Cys | His | Gly | Ala |    |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| tgg | att | tgg | cac | aaa | ctg | aaa | ccg | gcc | ctg | gaa | cgt | gct | ggc | cac | aaa | 96 |
| Trp | Ile | Trp | His | Lys | Leu | Lys | Pro | Ala | Leu | Glu | Arg | Ala | Gly | His | Lys |    |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ggt | act | gca | ctg | gac | atg | gca | gcc | agt | ggc | att | gac | ccg | cgt | caa | att | 144 |
| Val | Thr | Ala | Leu | Asp | Met | Ala | Ala | Ser | Gly | Ile | Asp | Pro | Arg | Gln | Ile |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gaa | cag | atc | aac | tct | ttc | gat | gaa | tac | tct | gaa | ccg | ctg | ctg | act | ttc | 192 |
| Glu | Gln | Ile | Asn | Ser | Phe | Asp | Glu | Tyr | Ser | Glu | Pro | Leu | Leu | Thr | Phe |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ctg | gaa | aaa | ctg | ccg | caa | ggc | gaa | aag | ggt | atc | att | ggt | ggt | gaa | agc | 240 |
| Leu | Glu | Lys | Leu | Pro | Gln | Gly | Glu | Lys | Val | Ile | Ile | Val | Gly | Glu | Ser |     |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tgt | gca | ggc | ctg | aac | att | gct | att | gct | gct | gat | cgt | tac | ggt | gac | aaa | 288 |
| Cys | Ala | Gly | Leu | Asn | Ile | Ala | Ile | Ala | Ala | Asp | Arg | Tyr | Val | Asp | Lys |     |

| 85  | 90  | 95  |     |
|---|-----|-----|-----|
| att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac |     |     | 336 |
| Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His |     |     |     |
| 100   | 105 | 110 |     |
| agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg |     |     | 384 |
| Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp |     |     |     |
| 115   | 120 | 125 |     |
| cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc |     |     | 432 |
| Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile |     |     |     |
| 130   | 135 | 140 |     |
| act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc |     |     | 480 |
| Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr |     |     |     |
| 145   | 150 | 155 | 160 |
| aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg ctg atg cgc aag |     |     | 528 |
| Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys |     |     |     |
| 165   | 170 | 175 |     |
| ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa |     |     | 576 |
| Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu |     |     |     |
| 180   | 185 | 190 |     |
| aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac |     |     | 624 |
| Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp |     |     |     |
| 195   | 200 | 205 |     |
| aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa |     |     | 672 |
| Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys |     |     |     |
| 210   | 215 | 220 |     |
| ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg |     |     | 720 |
| Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu |     |     |     |
| 225   | 230 | 235 | 240 |
| aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca |     |     | 768 |
| Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala |     |     |     |
| 245   | 250 | 255 |     |
| tac gct taa   |     |     | 777 |
| Tyr Ala   |     |     |     |

<210> 16

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving  
a replacement of Val by Leu at position 173

<400> 16

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala



<220>  
<223> Description of Artificial Sequence: primer

<220>  
<221> misc\_feature  
<222> (19)..(21)  
<223> n is a, c, g, or t

<400> 18  
cagagagccc ttgcgcatnn ncatttttgc cagttcatat tcgcc 45

<210> 19  
<211> 777  
<212> DNA  
<213> Manihot esculenta

<220>  
<221> CDS  
<222> (1)..(777)  
  
<220>  
<223> cDNA coding for Modified SHNL involving  
a replacement of Met by Leu at position 174

<400> 19  
atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
1 5 10 15  
  
tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
20 25 30  
  
gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
35 40 45  
  
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
50 55 60  
  
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
65 70 75 80  
  
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
85 90 95  
  
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
100 105 110  
  
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384  
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
115 120 125

|   |     |
|---|-----|
| cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc | 432 |
| Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile |     |
| 130 135 140   |     |
|   |     |
| act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc | 480 |
| Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr |     |
| 145 150 155 160   |     |
|   |     |
| aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt ttg cgc aag | 528 |
| Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Leu Arg Lys |     |
| 165 170 175   |     |
|   |     |
| ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa | 576 |
| Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu |     |
| 180 185 190   |     |
|   |     |
| aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac | 624 |
| Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp |     |
| 195 200 205   |     |
|   |     |
| aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa | 672 |
| Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys |     |
| 210 215 220   |     |
|   |     |
| ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg | 720 |
| Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu |     |
| 225 230 235 240   |     |
|   |     |
| aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca | 768 |
| Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala |     |
| 245 250 255   |     |
|   |     |
| tac gct taa   | 777 |
| Tyr Ala   |     |

<210> 20  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
       a replacement of Met by Leu at position 174

<400> 20  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
   1                  5                  10                  15  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
           20                  25                  30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
           35                  40                  45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
   50                  55                  60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
   65                  70                  75                  80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
                             85                            90                            95  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
                             100                            105                            110  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
                             115                            120                            125  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
                             130                            135                            140  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
                             145                            150                            155                            160  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Leu Arg Lys  
                             165                            170                            175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
                             180                            185                            190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
                             195                            200                            205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
                             210                            215                            220  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
                             225                            230                            235                            240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
                             245                            250                            255  
 Tyr Ala

<210> 21  
 <211> 777  
 <212> DNA  
 <213> Manihot esculenta

<220>  
 <221> CDS  
 <222> (1)..(777)

<220>  
 <223> cDNA coding for Modified SHNL(SHNL Actmt022-G12) involving  
           a replacement of Lys by Asn at position 21

<400> 21  
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
   1                            5                            10                            15  
  
 tgg att tgg cac aat ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
                             20                            25                            30  
  
 gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
                             35                            40                            45  
  
 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
                             50                            55                            60  
  
 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Glu | Lys | Leu | Pro | Gln | Gly | Glu | Lys | Val | Ile | Ile | Val | Gly | Glu | Ser |     |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| tgt | gca | ggc | ctg | aac | att | gct | att | gct | gct | gat | cgt | tac | gtt | gac | aaa | 288 |  |
| Cys | Ala | Gly | Leu | Asn | Ile | Ala | Ile | Ala | Ala | Asp | Arg | Tyr | Val | Asp | Lys |     |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| att | gca | gct | ggc | gtt | ttc | cac | aac | tcc | ctg | ctg | ccg | gac | acc | gtt | cac | 336 |  |
| Ile | Ala | Ala | Gly | Val | Phe | His | Asn | Ser | Leu | Leu | Pro | Asp | Thr | Val | His |     |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| agc | ccg | tct | tac | act | gtt | gaa | aag | ctg | ctg | gaa | tcg | ttc | ccg | gac | tgg | 384 |  |
| Ser | Pro | Ser | Tyr | Thr | Val | Glu | Lys | Leu | Leu | Glu | Ser | Phe | Pro | Asp | Trp |     |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| cgt | gac | aca | gaa | tat | ttc | acg | ttc | acc | aac | atc | act | ggc | gaa | acc | atc | 432 |  |
| Arg | Asp | Thr | Glu | Tyr | Phe | Thr | Phe | Thr | Asn | Ile | Thr | Gly | Glu | Thr | Ile |     |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |  |
| act | acc | atg | aaa | ctg | ggc | ttc | gtt | ctg | ctg | cgt | gaa | aac | ctg | ttc | acc | 480 |  |
| Thr | Thr | Met | Lys | Leu | Gly | Phe | Val | Leu | Leu | Arg | Glu | Asn | Leu | Phe | Thr |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |     |  |
| aaa | tgc | act | gat | ggc | gaa | tat | gaa | ctg | gca | aaa | atg | gtt | atg | cgc | aag | 528 |  |
| Lys | Cys | Thr | Asp | Gly | Glu | Tyr | Glu | Leu | Ala | Lys | Met | Val | Met | Arg | Lys |     |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| ggc | tct | ctg | ttc | caa | aac | gtt | ctg | gct | cag | cgt | ccg | aag | ttc | act | gaa | 576 |  |
| Gly | Ser | Leu | Phe | Gln | Asn | Val | Leu | Ala | Gln | Arg | Pro | Lys | Phe | Thr | Glu |     |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |  |
| aaa | ggc | tac | ggc | tct | atc | aag | aaa | gtt | tat | att | tgg | acc | gat | caa | gac | 624 |  |
| Lys | Gly | Tyr | Gly | Ser | Ile | Lys | Lys | Val | Tyr | Ile | Trp | Thr | Asp | Gln | Asp |     |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |  |
| aaa | ata | ttc | ctg | ccg | gac | ttc | caa | cgc | tgg | caa | att | gca | aac | tac | aaa | 672 |  |
| Lys | Ile | Phe | Leu | Pro | Asp | Phe | Gln | Arg | Trp | Gln | Ile | Ala | Asn | Tyr | Lys |     |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |  |
| ccg | gac | aag | gtt | tat | cag | gtt | caa | ggc | ggc | gat | cac | aag | ctg | cag | ctg | 720 |  |
| Pro | Asp | Lys | Val | Tyr | Gln | Val | Gln | Gly | Gly | Asp | His | Lys | Leu | Gln | Leu |     |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |     |  |
| aca | aaa | act | gaa | gaa | gta | gct | cac | att | ctg | caa | gaa | gtt | gct | gat | gca | 768 |  |
| Thr | Lys | Thr | Glu | Glu | Val | Ala | His | Ile | Leu | Gln | Glu | Val | Ala | Asp | Ala |     |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |
| tac | gct | taa |     |     |     |     |     |     |     |     |     |     |     |     |     | 777 |  |
| Tyr | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

<210> 22

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL(SHNL Actmt022-G12) involving  
a replacement of Lys by Asn at position 21

<400> 22

```

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala
 1           5           10           15
Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys
          20           25           30
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile
          35           40           45
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe
          50           55           60
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser
          65           70           75           80
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys
          85           90           95
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His
          100          105          110
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp
          115          120          125
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile
          130          135          140
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr
          145          150          155          160
Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys
          165          170          175
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu
          180          185          190
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp
          195          200          205
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys
          210          215          220
Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu
          225          230          235          240
Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala
          245          250          255
Tyr Ala

```

<210> 23

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc\_feature

<222> (19)..(21)

<223> n is a, c, g, or t

<400> 23

ggcgcatgga tttggcacnn nctgaaaccg gccctggaa

<210> 24  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<220>  
 <221> misc\_feature  
 <222> (19)..(21)  
 <223> n is a, c, g, or t

<400> 24  
 ttccagggcc ggtttcagnn ngtgccaaat ccatgcgcc 39

<210> 25  
 <211> 777  
 <212> DNA  
 <213> Manihot esculenta

<220>  
 <221> CDS  
 <222> (1)..(777)

<220>  
 <223> cDNA coding for Modified SHNL involving  
 a replacement of Lys by Glu at position 21

<400> 25  
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15

tgg att tgg cac gaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
 Trp Ile Trp His Glu Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

| 100   | 105 | 110 |     |
|---|-----|-----|-----|
| agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg |     |     | 384 |
| Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp |     |     |     |
| 115   | 120 | 125 |     |
| cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc |     |     | 432 |
| Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile |     |     |     |
| 130   | 135 | 140 |     |
| act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc |     |     | 480 |
| Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr |     |     |     |
| 145   | 150 | 155 | 160 |
| aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag |     |     | 528 |
| Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys |     |     |     |
| 165   | 170 | 175 |     |
| ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa |     |     | 576 |
| Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu |     |     |     |
| 180   | 185 | 190 |     |
| aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac |     |     | 624 |
| Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp |     |     |     |
| 195   | 200 | 205 |     |
| aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa |     |     | 672 |
| Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys |     |     |     |
| 210   | 215 | 220 |     |
| ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg |     |     | 720 |
| Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu |     |     |     |
| 225   | 230 | 235 | 240 |
| aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca |     |     | 768 |
| Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala |     |     |     |
| 245   | 250 | 255 |     |
| tac gct taa   |     |     | 777 |
| Tyr Ala   |     |     |     |

<210> 26  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
 a replacement of Lys by Glu at position 21

<400> 26  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 Trp Ile Trp His Glu Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile



|   |     |
|---|-----|
| gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc | 192 |
| Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe |     |
| 50 55 60  |     |
| ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc | 240 |
| Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser |     |
| 65 70 75 80   |     |
| tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa | 288 |
| Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys |     |
| 85 90 95  |     |
| att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac | 336 |
| Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His |     |
| 100 105 110   |     |
| agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg | 384 |
| Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp |     |
| 115 120 125   |     |
| cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc | 432 |
| Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile |     |
| 130 135 140   |     |
| act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc | 480 |
| Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr |     |
| 145 150 155 160   |     |
| aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag | 528 |
| Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys |     |
| 165 170 175   |     |
| ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa | 576 |
| Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu |     |
| 180 185 190   |     |
| aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac | 624 |
| Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp |     |
| 195 200 205   |     |
| aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa | 672 |
| Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys |     |
| 210 215 220   |     |
| ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg | 720 |
| Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu |     |
| 225 230 235 240   |     |
| aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca | 768 |
| Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala |     |
| 245 250 255   |     |
| tac gct taa   | 777 |
| Tyr Ala   |     |

<211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
 a replacement of Lys by Asp at position 21

<400> 28  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 Trp Ile Trp His Asp Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255  
 Tyr Ala

<210> 29  
 <211> 777  
 <212> DNA  
 <213> Manihot esculenta

<220>  
 <221> CDS  
 <222> (1)..(777)

<220>  
 <223> cDNA coding for Modified SHNL involving  
 a replacement of Lys by Asn at position 21

<400> 29

|   |     |
|---|-----|
| atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca | 48  |
| Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala |     |
| 1 5 10 15   |     |
|   |     |
| tgg att tgg cac aac ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa | 96  |
| Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys |     |
| 20 25 30  |     |
|   |     |
| gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att | 144 |
| Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile |     |
| 35 40 45  |     |
|   |     |
| gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc | 192 |
| Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe |     |
| 50 55 60  |     |
|   |     |
| ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc | 240 |
| Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser |     |
| 65 70 75 80   |     |
|   |     |
| tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa | 288 |
| Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys |     |
| 85 90 95  |     |
|   |     |
| att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac | 336 |
| Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His |     |
| 100 105 110   |     |
|   |     |
| agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg | 384 |
| Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp |     |
| 115 120 125   |     |
|   |     |
| cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc | 432 |
| Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile |     |
| 130 135 140   |     |
|   |     |
| act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc | 480 |
| Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr |     |
| 145 150 155 160   |     |
|   |     |
| aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag | 528 |
| Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys |     |
| 165 170 175   |     |
|   |     |
| ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa | 576 |
| Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu |     |
| 180 185 190   |     |
|   |     |
| aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac | 624 |
| Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp |     |
| 195 200 205   |     |
|   |     |
| aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa | 672 |
| Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys |     |
| 210 215 220   |     |



ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255

tac gct taa 777  
 Tyr Ala

<210> 30

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving  
 a replacement of Lys by Asn at position 21

<400> 30

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Val Gly Glu Ser  
 65 70 75 80  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255  
 Tyr Ala

<210> 31  
 <211> 777  
 <212> DNA  
 <213> Manihot esculenta

<220>  
 <221> CDS  
 <222> (1)..(777)

<220>  
 <223> cDNA coding for Modified SHNL involving  
 replacement of Gly by Glu at position 165 and Val by Leu at position 173

<400> 31  
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95  
 att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
 100 105 110  
 agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
 115 120 125  
 cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
 130 135 140  
 act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160  
 aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg ctg atg cgc aag 528

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Cys | Thr | Asp | Glu | Glu | Tyr | Glu | Leu | Ala | Lys | Met | Leu | Met | Arg | Lys |     |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| ggc | tct | ctg | ttc | caa | aac | gtt | ctg | gct | cag | cgt | ccg | aag | ttc | act | gaa | 576 |  |
| Gly | Ser | Leu | Phe | Gln | Asn | Val | Leu | Ala | Gln | Arg | Pro | Lys | Phe | Thr | Glu |     |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |  |
| aaa | ggc | tac | ggc | tct | atc | aag | aaa | gtt | tat | att | tgg | acc | gat | caa | gac | 624 |  |
| Lys | Gly | Tyr | Gly | Ser | Ile | Lys | Lys | Val | Tyr | Ile | Trp | Thr | Asp | Gln | Asp |     |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |
| aaa | ata | ttc | ctg | ccg | gac | ttc | caa | cgc | tgg | caa | att | gca | aac | tac | aaa | 672 |  |
| Lys | Ile | Phe | Leu | Pro | Asp | Phe | Gln | Arg | Trp | Gln | Ile | Ala | Asn | Tyr | Lys |     |  |
|     | 210 |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |  |
| ccg | gac | aag | gtt | tat | cag | gtt | caa | ggc | ggc | gat | cac | aag | ctg | cag | ctg | 720 |  |
| Pro | Asp | Lys | Val | Tyr | Gln | Val | Gln | Gly | Gly | Asp | His | Lys | Leu | Gln | Leu |     |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |     |  |
| aca | aaa | act | gaa | gaa | gta | gct | cac | att | ctg | caa | gaa | gtt | gct | gat | gca | 768 |  |
| Thr | Lys | Thr | Glu | Glu | Val | Ala | His | Ile | Leu | Gln | Glu | Val | Ala | Asp | Ala |     |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |     |  |
| tac | gct | taa |     |     |     |     |     |     |     |     |     |     |     |     |     | 777 |  |
| Tyr | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

<210> 32  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
 replacement of Gly by Glu at position 165 and Val by Leu at position 173

<400> 32

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Val | Thr | Ala | His | Phe | Val | Leu | Ile | His | Thr | Ile | Cys | His | Gly | Ala |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Trp | Ile | Trp | His | Lys | Leu | Lys | Pro | Ala | Leu | Glu | Arg | Ala | Gly | His | Lys |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Val | Thr | Ala | Leu | Asp | Met | Ala | Ala | Ser | Gly | Ile | Asp | Pro | Arg | Gln | Ile |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Glu | Gln | Ile | Asn | Ser | Phe | Asp | Glu | Tyr | Ser | Glu | Pro | Leu | Leu | Thr | Phe |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Leu | Glu | Lys | Leu | Pro | Gln | Gly | Glu | Lys | Val | Ile | Ile | Val | Gly | Glu | Ser |  |  |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Cys | Ala | Gly | Leu | Asn | Ile | Ala | Ile | Ala | Ala | Asp | Arg | Tyr | Val | Asp | Lys |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Ile | Ala | Ala | Gly | Val | Phe | His | Asn | Ser | Leu | Leu | Pro | Asp | Thr | Val | His |  |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |  |
| Ser | Pro | Ser | Tyr | Thr | Val | Glu | Lys | Leu | Leu | Glu | Ser | Phe | Pro | Asp | Trp |  |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |  |
| Arg | Asp | Thr | Glu | Tyr | Phe | Thr | Phe | Thr | Asn | Ile | Thr | Gly | Glu | Thr | Ile |  |  |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |  |  |
| Thr | Thr | Met | Lys | Leu | Gly | Phe | Val | Leu | Leu | Arg | Glu | Asn | Leu | Phe | Thr |  |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |  |

Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys  
                   165                  170                  175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
                   180                  185                  190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
                   195                  200                  205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
                   210                  215                  220  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225                  230                  235                  240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
                   245                  250                  255  
 Tyr Ala

<210> 33  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 33  
 tatgaactgg caaaaatgct gctgcgcaag ggctctctgt tc 42

<210> 34  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 34  
 gaacagagag cccttgcgca gcagcatttt tgccagttca ta 42

<210> 35  
 <211> 777  
 <212> DNA  
 <213> Manihot esculenta

<220>  
 <221> CDS  
 <222> (1)..(777)

<220>  
 <223> cDNA coding for Modified SHNL involving replacement of Gly  
           by Glu at position 165 and Val by Leu at position 173 and  
           Met by Leu at position 174

<400> 35  
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

| 1   | 5   | 10 | 15 |  |
|---|-----|----|----|--|
| tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa | 96  |    |    |  |
| Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys |     |    |    |  |
| 20 25 30  |     |    |    |  |
| ggt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att | 144 |    |    |  |
| Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile |     |    |    |  |
| 35 40 45  |     |    |    |  |
| gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc | 192 |    |    |  |
| Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe |     |    |    |  |
| 50 55 60  |     |    |    |  |
| ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc | 240 |    |    |  |
| Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser |     |    |    |  |
| 65 70 75 80   |     |    |    |  |
| tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa | 288 |    |    |  |
| Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys |     |    |    |  |
| 85 90 95  |     |    |    |  |
| att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac | 336 |    |    |  |
| Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His |     |    |    |  |
| 100 105 110   |     |    |    |  |
| agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg | 384 |    |    |  |
| Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp |     |    |    |  |
| 115 120 125   |     |    |    |  |
| cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc | 432 |    |    |  |
| Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile |     |    |    |  |
| 130 135 140   |     |    |    |  |
| act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc | 480 |    |    |  |
| Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr |     |    |    |  |
| 145 150 155 160   |     |    |    |  |
| aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg ctg ctg cgc aag | 528 |    |    |  |
| Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Leu Arg Lys |     |    |    |  |
| 165 170 175   |     |    |    |  |
| ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa | 576 |    |    |  |
| Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu |     |    |    |  |
| 180 185 190   |     |    |    |  |
| aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac | 624 |    |    |  |
| Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp |     |    |    |  |
| 195 200 205   |     |    |    |  |
| aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa | 672 |    |    |  |
| Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys |     |    |    |  |
| 210 215 220   |     |    |    |  |
| ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg | 720 |    |    |  |
| Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu |     |    |    |  |
| 225 230 235 240   |     |    |    |  |

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
                   245                                  250                                  255

tac gct taa 777  
 Tyr Ala

<210> 36  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving replacement of Gly by Glu at  
           position 165 and Val by Leu at position 173 and Met by  
           Leu at position 174

<400> 36  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
   1                                  5                                  10                                  15  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
                                   20                                  25                                  30  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
                                   35                                  40                                  45  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
                                   50                                  55                                  60  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
                                   65                                  70                                  75                                  80  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
                                   85                                  90                                  95  
 Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
                                   100                                  105                                  110  
 Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
                                   115                                  120                                  125  
 Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
                                   130                                  135                                  140  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
                                   145                                  150                                  155                                  160  
 Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Leu Arg Lys  
                                   165                                  170                                  175  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
                                   180                                  185                                  190  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
                                   195                                  200                                  205  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
                                   210                                  215                                  220  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
                                   225                                  230                                  235                                  240  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
                                   245                                  250                                  255  
 Tyr Ala

<210> 37  
 <211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<220>  
<221> misc\_feature  
<222> (23)..(25)  
<223> n is a, c, g, or t

<400> 37  
tgaaaacctg ttcaccaaat gcnnngatgg cgaatatgaa ctggc 45

<210> 38  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<220>  
<221> misc\_feature  
<222> (21)..(23)  
<223> n is a, c, g, or t

<400> 38  
gccagttcat attcgccatc nnngcatttg gtgaacaggt tttca 45

<210> 39  
<211> 777  
<212> DNA  
<213> Manihot esculenta

<220>  
<221> CDS  
<222> (1)..(777)  
<223> cDNA coding for Modified SHNL involving  
a replacement of Thr by Asp at position 163

<400> 39  
atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Glu | Gln | Ile | Asn | Ser | Phe | Asp | Glu | Tyr | Ser | Glu | Pro | Leu | Leu | Thr | Phe |     |  |
| 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |  |
| ctg | gaa | aaa | ctg | ccg | caa | ggc | gaa | aag | gtt | atc | att | gtt | ggg | gaa | agc | 240 |  |
| Leu | Glu | Lys | Leu | Pro | Gln | Gly | Glu | Lys | Val | Ile | Ile | Val | Gly | Glu | Ser |     |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| tgt | gca | ggc | ctg | aac | att | gct | att | gct | gct | gat | cgt | tac | gtt | gac | aaa | 288 |  |
| Cys | Ala | Gly | Leu | Asn | Ile | Ala | Ile | Ala | Ala | Asp | Arg | Tyr | Val | Asp | Lys |     |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| att | gca | gct | ggc | gtt | ttc | cac | aac | tcc | ctg | ctg | ccg | gac | acc | gtt | cac | 336 |  |
| Ile | Ala | Ala | Gly | Val | Phe | His | Asn | Ser | Leu | Leu | Pro | Asp | Thr | Val | His |     |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| agc | ccg | tct | tac | act | gtt | gaa | aag | ctg | ctg | gaa | tcg | ttc | ccg | gac | tgg | 384 |  |
| Ser | Pro | Ser | Tyr | Thr | Val | Glu | Lys | Leu | Leu | Glu | Ser | Phe | Pro | Asp | Trp |     |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| cgt | gac | aca | gaa | tat | ttc | acg | ttc | acc | aac | atc | act | ggc | gaa | acc | atc | 432 |  |
| Arg | Asp | Thr | Glu | Tyr | Phe | Thr | Phe | Thr | Asn | Ile | Thr | Gly | Glu | Thr | Ile |     |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |  |
| act | acc | atg | aaa | ctg | ggg | ttc | gtt | ctg | ctg | cgt | gaa | aac | ctg | ttc | acc | 480 |  |
| Thr | Thr | Met | Lys | Leu | Gly | Phe | Val | Leu | Leu | Arg | Glu | Asn | Leu | Phe | Thr |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| aaa | tgc | gat | gat | ggc | gaa | tat | gaa | ctg | gca | aaa | atg | gtt | atg | cgc | aag | 528 |  |
| Lys | Cys | Asp | Asp | Gly | Glu | Tyr | Glu | Leu | Ala | Lys | Met | Val | Met | Arg | Lys |     |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |  |
| ggc | tct | ctg | ttc | caa | aac | gtt | ctg | gct | cag | cgt | ccg | aag | ttc | act | gaa | 576 |  |
| Gly | Ser | Leu | Phe | Gln | Asn | Val | Leu | Ala | Gln | Arg | Pro | Lys | Phe | Thr | Glu |     |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |  |
| aaa | ggc | tac | ggc | tct | atc | aag | aaa | gtt | tat | att | tgg | acc | gat | caa | gac | 624 |  |
| Lys | Gly | Tyr | Gly | Ser | Ile | Lys | Lys | Val | Tyr | Ile | Trp | Thr | Asp | Gln | Asp |     |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |
| aaa | ata | ttc | ctg | ccg | gac | ttc | caa | cgc | tgg | caa | att | gca | aac | tac | aaa | 672 |  |
| Lys | Ile | Phe | Leu | Pro | Asp | Phe | Gln | Arg | Trp | Gln | Ile | Ala | Asn | Tyr | Lys |     |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |  |
| ccg | gac | aag | gtt | tat | cag | gtt | caa | ggc | ggc | gat | cac | aag | ctg | cag | ctg | 720 |  |
| Pro | Asp | Lys | Val | Tyr | Gln | Val | Gln | Gly | Gly | Asp | His | Lys | Leu | Gln | Leu |     |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |  |
| aca | aaa | act | gaa | gaa | gta | gct | cac | att | ctg | caa | gaa | gtt | gct | gat | gca | 768 |  |
| Thr | Lys | Thr | Glu | Glu | Val | Ala | His | Ile | Leu | Gln | Glu | Val | Ala | Asp | Ala |     |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |
| tac | gct | taa |     |     |     |     |     |     |     |     |     |     |     |     |     | 777 |  |
| Tyr | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |



<211> 258  
<212> PRT  
<213> Manihot esculenta

<220>  
<223> Modified SHNL involving  
a replacement of Thr by Asp at position 163

<400> 40

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Asp Arg Tyr Val Asp Lys  
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
145 150 155 160

Lys Cys Asp Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255

Tyr Ala

<210> 41  
 <211> 777  
 <212> DNA  
 <213> Manihot esculenta

<220>  
 <221> CDS  
 <222> (1)..(777)  
 <223> cDNA coding for Modified SHNL involving  
 a replacement of Thr by Glu at position 163

<400> 41  
 atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
 Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15  
 tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
 Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30  
 gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
 Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45  
 gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
 Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
 50 55 60  
 ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
 Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
 65 70 75 80  
 tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
 Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
 85 90 95

|   |     |
|---|-----|
| att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac<br>Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His<br>100 105 110     | 336 |
| agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg<br>Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp<br>115 120 125     | 384 |
| cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc<br>Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile<br>130 135 140     | 432 |
| act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc<br>Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr<br>145 150 155 160 | 480 |
| aaa tgc gaa gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag<br>Lys Cys Glu Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys<br>165 170 175     | 528 |
| ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa<br>Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu<br>180 185 190     | 576 |
| aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac<br>Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp<br>195 200 205     | 624 |
| aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa<br>Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys<br>210 215 220     | 672 |
| ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg<br>Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu<br>225 230 235 240 | 720 |
| aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca<br>Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala<br>245 250 255     | 768 |
| tac gct taa<br>Tyr Ala  | 777 |

<210> 42  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
 a replacement of Thr by Glu at position 163

<400> 42

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | 5   | 10  | 15  |     |     |     |     |     |     |     |     |     |     |     |     |
| Trp | Ile | Trp | His | Lys | Leu | Lys | Pro | Ala | Leu | Glu | Arg | Ala | Gly | His | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Thr | Ala | Leu | Asp | Met | Ala | Ala | Ser | Gly | Ile | Asp | Pro | Arg | Gln | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Gln | Ile | Asn | Ser | Phe | Asp | Glu | Tyr | Ser | Glu | Pro | Leu | Leu | Thr | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Glu | Lys | Leu | Pro | Gln | Gly | Glu | Lys | Val | Ile | Ile | Val | Gly | Glu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Ala | Gly | Leu | Asn | Ile | Ala | Ile | Ala | Ala | Asp | Arg | Tyr | Val | Asp | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ala | Ala | Gly | Val | Phe | His | Asn | Ser | Leu | Leu | Pro | Asp | Thr | Val | His |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Ser | Pro | Ser | Tyr | Thr | Val | Glu | Lys | Leu | Leu | Glu | Ser | Phe | Pro | Asp | Trp |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Arg | Asp | Thr | Glu | Tyr | Phe | Thr | Phe | Thr | Asn | Ile | Thr | Gly | Glu | Thr | Ile |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Thr | Thr | Met | Lys | Leu | Gly | Phe | Val | Leu | Leu | Arg | Glu | Asn | Leu | Phe | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Cys | Glu | Asp | Gly | Glu | Tyr | Glu | Leu | Ala | Lys | Met | Val | Met | Arg | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Ser | Leu | Phe | Gln | Asn | Val | Leu | Ala | Gln | Arg | Pro | Lys | Phe | Thr | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Gly | Tyr | Gly | Ser | Ile | Lys | Lys | Val | Tyr | Ile | Trp | Thr | Asp | Gln | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Ile | Phe | Leu | Pro | Asp | Phe | Gln | Arg | Trp | Gln | Ile | Ala | Asn | Tyr | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Asp | Lys | Val | Tyr | Gln | Val | Gln | Gly | Gly | Asp | His | Lys | Leu | Gln | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
245 250 255

Tyr Ala

<210> 43  
<211> 777  
<212> DNA  
<213> Manihot esculenta

<220>  
<221> CDS  
<222> (1)..(777)  
<223> cDNA coding for Modified SHNL involving  
a replacement of Thr by Ser at position 163

<400> 43  
atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48  
Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
1 5 10 15  
  
tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96  
Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
20 25 30  
  
gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144  
Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
35 40 45  
  
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
50 55 60  
  
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
65 70 75 80  
  
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys  
85 90 95  
  
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
100 105 110  
  
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384  
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
115 120 125  
  
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432  
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480  
 Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
 145 150 155 160

aaa tgc tct gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528  
 Lys Cys Ser Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
 165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576  
 Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
 180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624  
 Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
 195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672  
 Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
 210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720  
 Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
 225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768  
 Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
 245 250 255

tac gct taa 777  
 Tyr Ala

<210> 44  
 <211> 258  
 <212> PRT  
 <213> Manihot esculenta

<220>  
 <223> Modified SHNL involving  
 a replacement of Thr by Ser at position 163

<400> 44

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala  
 1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys  
 20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile  
 35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe  
50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser  
65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Asp Arg Tyr Val Asp Lys  
85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His  
100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp  
115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile  
130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr  
145 150 155 160

Lys Cys Ser Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys  
165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu  
180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp  
195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys  
210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu  
225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala  
245 250 255

Tyr Ala